

1. (Amended) A method of assigning an individual to a population of origin, which comprises:

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- (a) identifying a set of candidate populations of origin, wherein each candidate population is characterized by genotype frequencies and allele frequencies at one or more marker loci;
 - (b) determining a population prior genotype probability for an individual and said each candidate population using knowledge concerning the individual which is available prior to genotyping the individual;
 - (c) genotyping the individual to identify alleles at the one or more marker loci in step (a) to thereby identify the individual's genotype;
 - (d) sequentially determining a population genotype probability for the individual and said each candidate population based on the genotype of the individual under a null hypothesis that the individual arose from said each candidate population;
 - (e) combining the population prior genotype probability from step (b) and the population genotype probability from step (d) to obtain a population posterior genotype probability for the individual and said each candidate population;
 - (f) identifying a most likely population of origin, wherein the most likely population of origin has the largest population posterior genotype probability among the set of candidate populations; and
 - (g) assigning the individual to the most likely population of origin identified in step (f).

2. (Amended) The method of claim 1, wherein the individual is only assigned to the most likely population of origin if the population posterior genotype probability for the most likely population of origin exceeds a threshold value.

3. (Amended) The method of claim 1, which further comprises:

(a) computing an additional probability with which genotypes rarer than the individual's genotype occur in the most likely population of origin; and

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(b) if the additional probability in step (a) is above a threshold value, assigning the individual to the most likely population of origin, or if the additional probability in step (a) is not above the threshold value, assigning the individual to a novel population that is not represented among the set of candidate populations of origin.

5. (Amended) The method of claim 4, wherein the threshold value is determined using population posterior genotype probabilities of a sample of individuals from said each candidate population who are independent of individuals used to characterize said each candidate population.

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6. (Amended) The method of claim 4, wherein the threshold value is varied to determine the percentage of a sample of individuals who a) cannot be classified, b) are correctly classified, and c) are incorrectly classified.

8. (Amended) The method of claim 7, wherein the threshold value is determined using population posterior genotype probabilities of a sample of individuals from said each candidate population who are independent of individuals used to characterize said each candidate population.

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9. (Amended) The method of claim 7, wherein the threshold value is increased to reduce the percentage of a sample of individuals who are incorrectly classified to one of the candidate populations of origin.

11. (Amended) The method of claim 10, wherein the one or more morphological features allow the exclusion of one or more of the candidate populations of origin.

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12. (Amended) The method of claim 11, wherein the one or more morphological features are selected from the group consisting of coat color, presence or absence of horns, presence or absence of a shoulder hump, and presence or absence of a long, downswep ear.

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14. (Amended) The method of claim 1, wherein the population prior genotype probability for the individual and said each candidate population is set to equal a proportion of total population size in said each candidate population.